OIPE

RAW SEQUENCE LISTING   DATE: 01/10/2002
PATENT APPLICATION: US/10/017,410   TIME: 15:52:34

Input Set : A:\Uw974011.app
Output Set: N:\CRF3\01102002\J017410.raw

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   3 <110> APPLICANT: Farnham, Peggy J
   4         Graveel, Carrie R
   6 <120> TITLE OF INVENTION: Polynucleotide Differentially Expressed in Liver Cancer
   8 <130> FILE REFERENCE: 960296.97401
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/017,410
C--> 11 <141> CURRENT FILING DATE: 2001-12-14
  13 <160> NUMBER OF SEQ ID NOS: 4
  15 <170> SOFTWARE: PatentIn Ver. 2.1
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  19 <212> TYPE: DNA
  20 <213> ORGANISM: Mus musculus
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  24 <222> LOCATION: (35)..(859)
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  31 gac cac ctg cgg gct ggc agt tcg gag gtg gat tgg tgc gag gac aac   103
  32 Asp His Leu Arg Ala Gly Ser Ser Glu Val Asp Trp Cys Glu Asp Asn
  33          10              15                  20
  35 tac act atc gtg cct gcc att gcc gag ttc tac aac acg atc agc aac   151
  36 Tyr Thr Ile Val Pro Ala Ile Ala Glu Phe Tyr Asn Thr Ile Ser Asn
  37      25              30                  35
  39 gtc ttg ttt ttc att tta cct ccc atc tgc atg tgc ttg ttc cgc cag   199
  40 Val Leu Phe Phe Ile Leu Pro Pro Ile Cys Met Cys Leu Phe Arg Gln
  41  40              45                  50                  55
  43 tac gca acg tgc ttc aac agc ggc atc tac tta ata tgg acg ctc cta   247
  44 Tyr Ala Thr Cys Phe Asn Ser Gly Ile Tyr Leu Ile Trp Thr Leu Leu
  45              60                  65                  70
  47 gtt gta gtg ggg att gga tct gtc tac ttc cat gca acg ctg agt ttc   295
  48 Val Val Val Gly Ile Gly Ser Val Tyr Phe His Ala Thr Leu Ser Phe
  49              75                  80                  85
  51 ctg ggt cag atg ctt gat gaa ctt gcc att ctg tgg gtt ctg atg tgt   343
  52 Leu Gly Gln Met Leu Asp Glu Leu Ala Ile Leu Trp Val Leu Met Cys
  53          90              95                  100
  55 gct ttg gcc atg tgg ttt ccc agg agg tat tta cca aag atc ttt cgg   391
  56 Ala Leu Ala Met Trp Phe Pro Arg Arg Tyr Leu Pro Lys Ile Phe Arg
  57      105             110                 115
  59 aat gac agg ggc agg ttc aag gca gtg gtg tgt gtc ctg tct gca att   439
  60 Asn Asp Arg Gly Arg Phe Lys Ala Val Val Cys Val Leu Ser Ala Ile
  61 120             125                 130                 135
  63 aca acg tgc ttg gcg ttt atc aag ccc gcc atc aac aat att tcc ctg   487
  64 Thr Thr Cys Leu Ala Phe Ile Lys Pro Ala Ile Asn Asn Ile Ser Leu
  65              140                 145                 150
  67 atg att ctg gga ctt cca tgc act gcg ctg ctt gtt gca gag ctg aag   535
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Input Set : **A:\Uw974011.app**
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68 Met Ile Leu Gly Leu Pro Cys Thr Ala Leu Leu Val Ala Glu Leu Lys
69               155                 160                 165
71 agg tgt gac aat gtg cgt gtg ttt aag ctg ggc ctc ttc tct ggc ctc   583
72 Arg Cys Asp Asn Val Arg Val Phe Lys Leu Gly Leu Phe Ser Gly Leu
73           170                 175                 180
75 tgg tgg act ctg gct ctc ttc tgc tgg atc agc gac caa gcc ttc tgt   631
76 Trp Trp Thr Leu Ala Leu Phe Cys Trp Ile Ser Asp Gln Ala Phe Cys
77     185                 190                 195
79 gag ctg ctc tcc tcc ttt cac ttc ccc tac ctg cac tgt gtg tgg cat   679
80 Glu Leu Leu Ser Ser Phe His Phe Pro Tyr Leu His Cys Val Trp His
81 200                 205                 210                 215
83 att ctc atc tgc ctt gct tcg tac ctg ggc tgt gtg tgc ttc gcc tac   727
84 Ile Leu Ile Cys Leu Ala Ser Tyr Leu Gly Cys Val Cys Phe Ala Tyr
85               220                 225                 230
87 ttt gat gct gcc tca gag ata cct gag caa ggt cca gtc atc aga ttc   775
88 Phe Asp Ala Ala Ser Glu Ile Pro Glu Gln Gly Pro Val Ile Arg Phe
89           235                 240                 245
91 tgg ccc agc gag aaa tgg gct ttt att ggt gtc cct tat gtg tcc ctt   823
92 Trp Pro Ser Glu Lys Trp Ala Phe Ile Gly Val Pro Tyr Val Ser Leu
93           250                 255                 260
95 ctg tgt gcc cac aag aag tcg cca gtc aag atc acg tgatggcaag       869
96 Leu Cys Ala His Lys Lys Ser Pro Val Lys Ile Thr
97         265                 270                 275
99  gcagtgacca gcttctctac ttacttctat tcgagtgcgc gctgggcttc gtttgctagc  929
101 aaagatggct gaggggggttg aggaattggt gtggtgtggg tgtttaaaat tctgctcctt  989
103 tgtgatctaa ctggaccact gtgcctgacc tccctaggtt aagtagaggg ctcagggaca 1049
105 taaggtgtct tcctcagtat cctttccagg catacgggct tgctgggtta tgtccataat 1109
107 gacatcaaca gagtagttct ttgggagacc tagggcaacc caaagtttct tgctggagag 1169
109 ggtagcttgc tgtttccacc atttccagac tctcaacccc ctgataaaca agaccttctg 1229
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121 gacccacaga gaatccttca ggttatgtga agattccaca cacagccccc tcttgtgacc 1589
123 tctgtgagag caaggcctcg ttgtaatcgc ggaggcagct ctggaggctt gactgtggag 1649
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129 cctccctagg atgtgggcct ccggcttttg ttttcataat acctggtgct aactggtttc 1829
131 tcagagcact ttgctcttct tgatgctggg cggtcactac actctgattg gctggctggg 1889
133 gatcccaggg aggaaggggc agactctgac atgaatgtct ctcacctgca tcctactgtc 1949
135 ttcactgggc tctcttcagg gtatgaagtg ggtatggggt atctcaggga tgtttgtaac 2009
137 tcaggcacct tctgctttct gacattccat tgtcagtggt gagactgcac tcaggggact 2069
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145 gtaacttgct gggctatttc ttgtttatag tcacaaatat ttatagaaca tgaaggtgta 2309
147 aaataagttg tcttttatta aattcatagc atttaccaac tctcccaggt agcaaacaca 2369
149 cagtcatttg attggcgatt tacaaggcag gaatacttgg ttttgaatga ttgtatatgt 2429
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151 cattttactg tagcttaaaa tatgtttaaa atgactttga gtgaaatgtt tgtggcaacc 2489
153 taggggttta tggatcagaa ttgcggctga gtcctttggt ttttgagtct agaagttttc 2549
155 agagggcaaa atcaaactag ccttgtttct ggttcatctt accaggctcg ggagctgccc 2609
157 ttatatattc tacataagga cttattatac ataagtctgt ataaatgtcc tgaagatgac 2669
159 acctagctgc cttcatctgg aagggtcgtc tggggctgga gagttggttc aacagttaag 2729
161 aacccgtgtt gctctctccc agacgaccca gcgacttgtg aggctcataa ccagcaactc 2789
163 cagccctggg gcatctgacg ccctcttctg acttctaagg gcatttggtg cacacgtaca 2849
165 tacaggcagg caaaacattt atacatgtaa cgtaataaat gcataagtta gtgagacggc 2909
167 tgaaggaaag gagttttaga tgcaaggttt agtctgacct gagtgccctt ccttagccgc 2969
169 gatggtgtcc tcaaagtcag ggaagaacca tttctttttt atcaggaaaa ggacttattc 3029
171 cctagggcct ctgctgacat ccctaggaac agagataaaa tacggatgga tgtgaatgaa 3089
173 catgcttggg tgaaaggagc cgagtacctg actggaccca gtgggccact tccacaagcg 3149
175 aagcccggta accgatgtgc actccagaat cttctccctt ctggtagaga tgacatcgat 3209
177 gagtgatgtc gtgaccactg ggccctgcat gggtgtcggg ctctgttctg ttccgaatct 3269
179 acctgagatc tcaggacaga ggaagccatg aatgttacca agtggtcatg gctgtcagtg 3329
181 attttacagt tttgaaccat tattggtttt taggagaatt cttctctctc tagtgccctg 3389
183 tgatgccaaa gccagccctt cagaagtgtt ccttctgtct gcttcccttt gtaatgtgat 3449
185 ccactcgggg aaatgggtgt ctacccaggg aaaagtgcct accccagtca cgggtcaaca 3509
187 gtgttgtgtt gaggatcaaa catggctctg tgaaaatact gccacccatt ctattggttg 3569
189 gatttctcag gagtctgaat cttccctcac gagtcctctt ctcccaaccc ctacccagag 3629
191 ccaacactgg gatttgaacc ttctctgact ctcttcttcc ctcaggtctg acaactaatg 3689
193 gtctctgggg acacccagct agggccttcc ccaactcctt atccagctga acttggattc 3749
195 ttcccaacca gggcttgacc tgggtgctgt tggtcccact ggccaacaac acatctttgg 3809
197 ccagattggg attctcaata gattttatag acattattct cccacagact ttaaaacatg 3869
199 gcttgtgtct ttccatacac atccggtcag atttaaaact attttataac cacaggaatt 3929
201 aaaccaagca aatagagtac tttcagatat aaactgtgtt tcatacttta tgtagagtgt 3989
203 gctatgtata ggcggtatgt accctggctg aagtaatatt aaccatagct ctgggaggat 4049
205 ttacagacct tttgcacttt atgctttttt gtgaactctg ataaccatgg tcaatattaa 4109
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209 aaaaac                                                          4175
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213 <211> LENGTH: 275
214 <212> TYPE: PRT
215 <213> ORGANISM: Mus musculus
217 <400> SEQUENCE: 2

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222              20                  25                  30
224 Phe Tyr Asn Thr Ile Ser Asn Val Leu Phe Phe Ile Leu Pro Pro Ile
225          35                  40                  45
227 Cys Met Cys Leu Phe Arg Gln Tyr Ala Thr Cys Phe Asn Ser Gly Ile
228      50                  55                  60
230 Tyr Leu Ile Trp Thr Leu Leu Val Val Val Gly Ile Gly Ser Val Tyr
231  65                  70                  75                  80
233 Phe His Ala Thr Leu Ser Phe Leu Gly Gln Met Leu Asp Glu Leu Ala
234              85                  90                  95
236 Ile Leu Trp Val Leu Met Cys Ala Leu Ala Met Trp Phe Pro Arg Arg
237              100                 105                 110
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239 Tyr Leu Pro Lys Ile Phe Arg Asn Asp Arg Gly Arg Phe Lys Ala Val
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243         130                 135                 140
245 Ala Ile Asn Asn Ile Ser Leu Met Ile Leu Gly Leu Pro Cys Thr Ala
246 145                 150                 155                 160
248 Leu Leu Val Ala Glu Leu Lys Arg Cys Asp Asn Val Arg Val Phe Lys
249         165                 170                 175
251 Leu Gly Leu Phe Ser Gly Leu Trp Trp Thr Leu Ala Leu Phe Cys Trp
252         180                 185                 190
254 Ile Ser Asp Gln Ala Phe Cys Glu Leu Leu Ser Ser Phe His Phe Pro
255         195                 200                 205
257 Tyr Leu His Cys Val Trp His Ile Leu Ile Cys Leu Ala Ser Tyr Leu
258     210                 215                 220
260 Gly Cys Val Cys Phe Ala Tyr Phe Asp Ala Ala Ser Glu Ile Pro Glu
261 225                 230                 235                 240
263 Gln Gly Pro Val Ile Arg Phe Trp Pro Ser Glu Lys Trp Ala Phe Ile
264                 245                 250                 255
266 Gly Val Pro Tyr Val Ser Leu Leu Cys Ala His Lys Lys Ser Pro Val
267             260                 265                 270
269 Lys Ile Thr
270             275
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275 <211> LENGTH: 828
276 <212> TYPE: DNA
277 <213> ORGANISM: Homo sapiens
279 <220> FEATURE:
280 <221> NAME/KEY: CDS
281 <222> LOCATION: (1)..(825)
283 <400> SEQUENCE: 3
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286  1               5                  10                  15
288 gtg gac tgg tgc gag gac aac tac acc atc gtg cct gct atc gcc gag   96
289 Val Asp Trp Cys Glu Asp Asn Tyr Thr Ile Val Pro Ala Ile Ala Glu
290             20                  25                  30
292 ttc tac aac acg atc agc aat gtc tta ttt ttc att tta ccg ccc atc  144
293 Phe Tyr Asn Thr Ile Ser Asn Val Leu Phe Phe Ile Leu Pro Pro Ile
294         35                  40                  45
296 tgc atg tgc ttg ttt gat gag tat gca aca tgc ttg aac agt gac atc  192
297 Cys Met Cys Leu Phe Asp Glu Tyr Ala Thr Cys Leu Asn Ser Asp Ile
298     50                  55                  60
300 tac tta atc tgg act ctt ttg gtt gta gtg gga att gga tcc gtc tac  240
301 Tyr Leu Ile Trp Thr Leu Leu Val Val Val Gly Ile Gly Ser Val Tyr
302 65                  70                  75                  80
304 ttc cat ttt acc ctt agt ttc ttg ggt cag atg ctt gat gaa ctt gca  288
305 Phe His Phe Thr Leu Ser Phe Leu Gly Gln Met Leu Asp Glu Leu Ala
306             85                  90                  95
308 gtc ctt tgg gtt ctg atg tgt gct ttg gcc atg tgg ttc ccc aga agg  336
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309 Val Leu Trp Val Leu Met Cys Ala Leu Ala Met Trp Phe Pro Arg Arg
310             100             105             110
312 tat cta cca aag atc ttt cgg aat gac agg ggt agg ttc aag gtg gtg   384
313 Tyr Leu Pro Lys Ile Phe Arg Asn Asp Arg Gly Arg Phe Lys Val Val
314             115             120             125
316 gtc agt gtc ctg tct gcg gtt acg acg tgc ctg gca ttt gtc aag cct   432
317 Val Ser Val Leu Ser Ala Val Thr Thr Cys Leu Ala Phe Val Lys Pro
318             130             135             140
320 gcc atc aac aac atc tct ctg atg acc ctg gga gtt cct tgc act gca   480
321 Ala Ile Asn Asn Ile Ser Leu Met Thr Leu Gly Val Pro Cys Thr Ala
322 145             150             155             160
324 ctg ctc atc gca gag cta aag agg tgt gac aac atg cgt gtg ttt aag   528
325 Leu Leu Ile Ala Glu Leu Lys Arg Cys Asp Asn Met Arg Val Phe Lys
326             165             170             175
328 ctg ggc ctc ttc tcg ggc ctc tgg tgg acc ctg gcc ctg ttc tgc tgg   576
329 Leu Gly Leu Phe Ser Gly Leu Trp Trp Thr Leu Ala Leu Phe Cys Trp
330             180             185             190
332 atc agt gac cga gct ttc tgc gag ctg ctg tca tcc ttc aac ttc ccc   624
333 Ile Ser Asp Arg Ala Phe Cys Glu Leu Leu Ser Ser Phe Asn Phe Pro
334             195             200             205
336 tac ctg cac tgc atg tgg cac atc ctc atc tgc ctt gct gcc tac ctg   672
337 Tyr Leu His Cys Met Trp His Ile Leu Ile Cys Leu Ala Ala Tyr Leu
338             210             215             220
340 ggc tgt gta tgc ttt gcc tac ttt gat gct gcc tca gag att cct gag   720
341 Gly Cys Val Cys Phe Ala Tyr Phe Asp Ala Ala Ser Glu Ile Pro Glu
342 225             230             235             240
344 caa ggc cct gtc atc aag ttc tgg ccc aat gag aaa tgg gcc ttc att   768
345 Gln Gly Pro Val Ile Lys Phe Trp Pro Asn Glu Lys Trp Ala Phe Ile
346             245             250             255
348 ggt gtc ccc tat gtg tcc ctc ctg tgt gcc aac aag aaa tca tca gtc   816
349 Gly Val Pro Tyr Val Ser Leu Leu Cys Ala Asn Lys Lys Ser Ser Val
350             260             265             270
352 aag atc acg tga                                                    828
353 Lys Ile Thr
354             275
357 <210> SEQ ID NO: 4
358 <211> LENGTH: 275
359 <212> TYPE: PRT
360 <213> ORGANISM: Homo sapiens
362 <400> SEQUENCE: 4
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367             20             25             30
369 Phe Tyr Asn Thr Ile Ser Asn Val Leu Phe Phe Ile Leu Pro Pro Ile
370             35             40             45
372 Cys Met Cys Leu Phe Asp Glu Tyr Ala Thr Cys Leu Asn Ser Asp Ile
373   50             55             60
375 Tyr Leu Ile Trp Thr Leu Leu Val Val Val Gly Ile Gly Ser Val Tyr
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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date